## EXHIBIT D 09/843,159

scoring	- 1						
scoring	ID NO:1					045 nt 797 nt	vs.
	g matrix: identity;	, gap pena	alties: -1 Global al:	2/-2 ignment sc	ore: -50	07	
		10			20	20	
778106	ATGG	CGGAGT		-CTTCGGAT	AAGCTCTA		
			rcatactttt				
_	1		20		40	50	TCACTACA
	40	50			60		
778106	GCCAAG-						
			: :: GAGCAGATCT				$CC\Delta CTTT\Delta$
				90		110	CCAGIIIA
	7	0 - 1	80	90	100		
778106	AGAAA'					GATG	GCCA
			: :				
-			ATAGATGTGG				GTCACTGT
1.	20 1	30	140	150	160	170	
		120					50
778106	-TCATGG						
		-	::: ::: :::				
- 1:	ATCATAAGG BO 1		ACATATTTAA 200			230	
-	-						
			170				
778106	TACCACT		CTTCTGGA				CTGA-CGT
	CATACTAAA						
		TATGCAGAA	CTCTATTGT	GAGTGAGAA.	ACATT	"I'GA-ACT	TTGAGCTT
-		250			ACATT 280		290
-	240	250	260	270	280	)	290
	210	250	260	270 230	280 240	)	290 250
	240	250	260 220 IGGGTTCTCI	270 230	280 240 TGGGATGA	) ATCAGC	290 250
	210 TGAGG : :: TCAGTCACT	250 TGGA' :: : TATTTTGTA'	260  220  TGGGTTCTC1 : :::::  TTCTTTCTT1	270 230 GAGCTTCGG ::::::::	280 240 TGGGATGA : : :	TCAGC ::: CCACCCA	290 250 AGAAAGTC :: : : AGGCACTG
	210 TGAGG	250 TGGA' :: : TATTTTGTA'	260 220 IGGGTTCTCI : :::::	270 230 'GAGCTTCGG' ::: :: :	280 240 TGGGATGA : : :	TCAGC	290 250 AGAAAGTC :: : :
	210 TGAGG: ::: TCAGTCACT 300	250 TGGA :: : TATTTTGTA' 310	260  220  TGGGTTCTC1 : :::::  TTCTTTCTT1	270 230 CGAGCTTCGG ::: :: :: CGAGGTTAGC. 330	280 240 TGGGATGA : : : AGTAGT-A	ATCAGC :: : ACCACCCA 340	290 250 AGAAAGTC :: : : AGGCACTG 350
778106	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC	250TGGA' :::: TATTTTGTA' 310 270 AGCGGAAGC'	260  220 TGGGTTCTCT : ::::: TTCTTTCTTT 320  280 TG-GAGGAGT	270 230 CGAGCTTCGG CCCCCCCCCCCCCCCCCCCCCCCCCCCC	240 TGGGATGA : : : AGTAGT-A 3 AGGC	ATCAGC :::: ACCACCCA 440	290 250 AGAAAGTC :: :: AGGCACTG 350
778106	210 TGAGG::: TCAGTCACT 300 260 AAGAAG-AC	250TGGA :::: TATTTTGTA 310 270 AGCGGAAGC :::::	260  220  TGGGTTCTCT : :::::  TTCTTTCTTT  320  280  TG-GAGGAGT : :::::	270 230 CGAGCTTCGG ::: :: : CGAGGTTAGC 330 290 CGACAGGCAA :: : :	240 TGGGATGA : : : AGTAGT-A 3 AGGC	ATCAGC :::: ACCACCCA 300CAGGAT :::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::::
778106	210 TGAGG : :: TCAGTCACT 300 260 AAGAAG-AC : : :: CTTAGGTAC	250 TGGA :::: TATTTTGTA 310  270 AGCGGAAGC ::::: CACTGCTGC	260  220  TGGGTTCTCT : :::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTGGAG	270 230 CGAGCTTCGG ::::::: CGAGGTTAGC 330 290 CGACAGGCAA ::::::	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA	TCAGC :::: ACCACCA 300CAGGAT ::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: :::: GGTTTTGG
778106	210 TGAGG::: TCAGTCACT 300 260 AAGAAG-AC	250TGGA :::: TATTTTGTA 310 270 AGCGGAAGC :::::	260  220  TGGGTTCTCT : :::::  TTCTTTCTTT  320  280  TG-GAGGAGT : :::::	270 230 CGAGCTTCGG ::::::: CGAGGTTAGC 330 290 CGACAGGCAA ::::::	240 TGGGATGA : : : AGTAGT-A 3 AGGC	ATCAGC :::: ACCACCCA 300CAGGAT :::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::::
778106 - 778106 -	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC ::::: CTTAGGTAC	250 TGGA :::: TATTTTGTA 310  270 AGCGGAAGC ::::: CACTGCTGC	260  220  TGGGTTCTCT : :::::  TTCTTTCTTT 320  280  TG-GAGGAGT : :::::  TTAGTGGAGF 380	270 230 CGAGCTTCGG ::::::: CGAGGTTAGC 330 290 CGACAGGCAA ::::::	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA	TCAGC :::: ACCACCA 300CAGGAT ::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: :::: GGTTTTGG
778106 - 778106 -	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC	250TGGA :::: TATTTTGTA 310 270 AGCGGAAGC ::::: CACTGCTGC 370 320 AGAGAAGAC	260  220  TGGGTTCTCT : :::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGF 380  330  TCTGGGTGAG	270 230 CGAGCTTCGG ::::::: CGAGGTTAGC 330 290 CGACAGGCAA ::::: GGTCCCTC 3 340 CTTTGCAG	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: :::: GGTTTTGG 410  360CCAACA
778106 - 778106 -	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::	250TGGA' ::::: TATTTTGTA' 310 270 AGCGGAAGC' :::::: CACTGCTGC' 370 320 AGAGAAGAC' :::::::	260  220  TGGGTTCTCT : :::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGA 380  330  TCTGGGTGAC : ::::	270 230 CGAGCTTCGG ::::::: CGAGGTTAGC 330 290 CGACAGGCAA :::::: GGTCCCTC 3 340 CTTTGCAG ::::::	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT	ATCAGC :::: ACCACCCA 300 -CAGGAT :::: ATCATTAA 400 CGCCAAGT :::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA ::::
778106 - 778106 -	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::	250TGGA' ::::: TATTTTGTA' 310 270 AGCGGAAGC' :::::: CACTGCTGC' 370 320 AGAGAAGAC' :::::::	260  220  TGGGTTCTCT : :::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGF 380  330  TCTGGGTGAG	270 230 CAGCTTCGG CONTROL CONT	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG	ATCAGC :::: ACCACCCA 300 -CAGGAT :::: ATCATTAA 400 CGCCAAGT :::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA ::::
778106 - 778106 -	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::	250TGGA' :: : TATTTTGTA' 310  270 AGCGGAAGC' : : :: CACTGCTGC' 370  320 AGAGAAGAC' : : :::: GGA-AAGAC	260  220  TGGGTTCTCT : ::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGAGA 380  330  TCTGGGTGAC : ::::  G-TAGTTGAF	270 230 CAGCTTCGG CONTROL CONT	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 CGCCAAGT ::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA :::: GTCCAA
778106 - 778106 - 778106	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::GC	250TGGA :::: TATTTTGTA 310 270 AGCGGAAGC ::::: CACTGCTGC 370 320 AGAGAAGAC :::::: GGA-AAGAC 420 380	260  220  TGGGTTCTCT : ::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGAGA 380  330  TCTGGGTGAC : ::::  G-TAGTTGAA 430	270 230 CGAGCTTCGG ::::::: CGAGGTTAGC 330 290 CGACAGGCAA ::::: GGTCCCTC 3 340 CTTTGCAG ::::: CTATTTGCTT 44 390	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG 0 400	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 CGCCAAGT :::: ETGCAAGT 450 410	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA :::: GTCCAA 460
778106 - 778106 - 778106	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::GC	250TGGA' :: : TATTTTGTA' 310 270 AGCGGAAGC' : : :: CACTGCTGC' 370 320 AGAGAAGAC' : : :::: GGA-AAGAC' 420 380 GCAAGGG	260  220  TGGGTTCTCT : ::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGAGA 380  330  TCTGGGTGAC : ::::  G-TAGTTGAF 430  GTGTATC	270 230 GAGCTTCGG ::::::: GAGGTTAGC 330 290 GACAGGCAA :::: GTCCCTC 3 40 CTTTGCAG ::::: CTATTTGCTT 44 390 GAGAAGATA	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG 0 400 GAAAAGGG	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 -CGCCAAGT ::::: ATGCAAGT 450 410 GCCAGGTG	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA :::: GTCCAA 460  GCGCCTGTC
778106 - 778106 - 778106	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::GC 370 GAAGTACGT :::::	250TGGA' :: : TATTTTGTA' 310 270 AGCGGAAGC' : : :: CACTGCTGC' 370  320 AGAGAAGAC' : : :::: GGA-AAGAC' 420  380 GCAAGGG' : : :::	260  220  TGGGTTCTCT : ::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGAGA 380  330  TCTGGGTGAC : ::::  G-TAGTTGAA 430	270 230 GAGCTTCGG ::::::: GAGGTTAGC 330 290 GACAGGCAA :::: GTCCCTC 3 40 CTTTGCAG ::::: CTATTTGCTT 44 390 GAGAAGATA ::::	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG 0 400 GAAAAGGG	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 -CGCCAAGT ::::: ATGCAAGT 450 410 GCCAGGTG ::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA :::: GTCCAA 460  CGCCTGTC ::::
778106 - 778106 - 778106	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::GC 370 GAAGTACGT :::::	250TGGA' :: : TATTTTGTA' 310 270 AGCGGAAGC' : : :: CACTGCTGC' 370  320 AGAGAAGAC' : : :::: GGA-AAGAC' 420  380 GCAAGGG' : : :::	260  220  TGGGTTCTCT : ::::  TTCTTTCTTT 320  280  TG-GAGGAGT : ::::  TTAGTTGGAGAGA 380  330  TCTGGGTGAC : ::::  G-TAGTTGAF 430  GTGTATC : : ::	270 230 CAGACTTCGG CI:::::: CAGGTTAGC 330 CACAGGCAA CI:::: CAGTCCCTC 3 40 CTTTGCAG CI:::: CATATTTGCTT 44 390 CAGAGAAGATA CI::: CCTCTTCATA	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG 0 400 GAAAAGGG	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 -CGCCAAGT ::::: ATGCAAGT 450 410 GCCAGGTG ::::	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA :::: GTCCAA 460  GCGCCTGTC ::: GTCATGCT
778106  - 778106  - 778106  - 778106	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::GC	250TGGA' :::: TATTTTGTA' 310 270 AGCGGAAGC' ::::: CACTGCTGC' 370  320 AGAGAAGAC' ::::::: GGA-AAGAC' 420 380 GCAAGGG' :::::: GATGATGGG' 470	260  220 TGGGTTCTCT : :::: TTCTTTCTTT 320  280 TG-GAGGAGT : :::: TTAGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	270 230 CGAGCTTCGG CI:::::: CGAGGTTAGC 330 CGACAGGCAA CI::: CGTCCCTC 3 340 CTTTGCAG CI:::: CTATTTGCTT 44 390 CGAGAAGATA CI::: CCTCTTCATA 490	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG 0 400 GAAAAGGG :: ATGCATGC	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 -CGCCAAGT :::: ATGCAAGT 450 410 GCCAGGTG ::: CTCTTTTG 51	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360 P-CCAACA :::: GTCCAA 460  GCGCCTGTC ::: GTCATGCT 0
778106  - 778106  - 778106  - 778106  - 4	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::GC 370 GAAGTACGT :::::GCACGT	250TGGA' :::: TATTTTGTA' 310 270 AGCGGAAGC' ::::: CACTGCTGC' 370  320 AGAGAAGAC' :::::: GGA-AAGAC' 420 380 GCAAGGG' ::::: GATGATGGG' 470  43	260  220 TGGGTTCTCT : :::: TTCTTTCTTT 320  280 TG-GAGGAGT : :::: TTAGTGGAGA 380  330 TCTGGGTGAC : :::: G-TAGTTGAF 430  GTGTATC : : : GGCCTTATC 480	270 230 CGAGCTTCGG 231 CGAGGTTAGC 330 CGACAGGCAA 2 : : : CGTCCCTC 3 340 CTTTGCAG 2 : : :: CTATTTGCTT 44 390 CGAGAAGATA 2 : : : CCTCTTCATA 490	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG 0 400 GAAAAGGG :: ATGCATGC 500 450	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 -CGCCAAGT ::::: GTGCAAGT 450 410 GCCAGGTG :::: CTCTTTTG 51	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA :::: GTCCAA 460  CCGCCTGTC :::: GTCATGCT 0
778106  - 778106  - 778106  - 778106  - 4	210 TGAGG ::: TCAGTCACT 300 260 AAGAAG-AC :::: CTTAGGTAC 360 310 TAGCAAGGC ::GC	250TGGA' :::: TATTTTGTA' 310 270 AGCGGAAGC' ::::: CACTGCTGC' 370 320 AGAGAAGAC' :::::: GGA-AAGAC' 420 380 GCAAGGG' ::::: GATGATGGG' 470 43TG'	260  220 TGGGTTCTCT : :::: TTCTTTCTTT 320  280 TG-GAGGAGT : :::: TTAGTGGAGA 380  330 TCTGGGTGAC : :::: G-TAGTTGAF 430  GTGTATC : : : GGCCTTATC 480	270 230 CGAGCTTCGG ::::::: CGAGGTTAGC 330  290 CGACAGGCAA :::: CGTCCCTC 3 340 CTTTGCAG ::::: CTATTTGCTT 44 390 CGAGAAGATA ::: CCTCTTCATA 490  440 CGAGAAGAGA	240 TGGGATGA : : : AGTAGT-A 3 AGGC ::: TGGCTTTA 90 350 CAGAGTAT :::: CAGAATGG 0 400 GAAAAGGG :: ATGCATGC 500 450 CCACAGCT	ATCAGC ::: ACCACCCA 300 -CAGGAT ::: ATCATTAA 400 -CGCCAAGT :::: ATGCAAGT 450 410 GCCAGGTG ::: CTCTTTTG 51 46 CAGGCATG	290 250 AGAAAGTC :: :: AGGCACTG 350  GGAATTGG :: ::: GGTTTTGG 410  360CCAACA :::: GTCCAA 460  CCGCCTGTC :::: GTCATGCT 0

	520	530	540	550	560	570
770106					510	520 TTCCGGCCCGAGT
778106	: ::			: :::::		:::
_	TATACTCCT	CTCCATGAA 590	GCTGCA 600		AGATTGATGT 620	TTGC
778106		AGTCAGCTCA	AGGGCTTCA	GCCTC		AGGATAAAGA-AG
					: ::::: CGAAATACAG	: : :: :: ATGG-AAGGACAG
_	630	640	650			680
		590			10 6	
778106					GAGTGAAGGA : :: ::	AAGAGAAAAGGCG
-			CATCTGCCA		TACTGGTGAA	TATAAGAAAGATG
779106	640		60 6		6 A	
770100				: : ::::::		:::: :
_		GAAAGTGC 76			AAAATGATGG 80 7	CTCTACTCACACC 90 800
778106					720 TAAAGGCTCA	730 GAACGACCTGATC
		::: :			:::: :::	
_	810			830	GAAAGTCA 840	ACTCCATTACATT 850
778106						780 790 -ACCTGAAGGAGC
						:: :: :: :
-	860 860		CAGAGTAAA ) 88			AACATGGAGCTGA 0 910
	-					840
778106	TACTCATC			AGTGCCTTCT		CGATCTTGGAC
	TGTCCATG	CTAAAGATAA	AGGTGATCT	GGTACCAT-T	ACACAATGCC	TGTTCTTATGGTC
	920	930	94	0 9	50 9	60 970
779106	CC7(	850	860		880	890 TGCGAGGAATGCT
778100	:	::: :::	::::	: :::::	::::	::: : : ::
-	ATTATGAA 980		CTTTTGGTCA 00 10			TGCAATGGACT 020
	900	91	.0 9	20 9	30 9	40 950
778106					ACTGCACTGG	GGACGTCACTGC-
- 1	TGTGGCAA		CTTCATGAG-		AGAACAGGGT	TGAAGTATGTTCT
778106				980 GACACC===C		AAG <b></b>
	:: :	: ::::::	:::::::	:::: :	:: :	:::
					AATTGTCACA 1130	ATAAAAGTGCTAT 1140
778106						0 1050 AATTGAAGGTTAA

	AGACTTGGCTCC	CACACCACAG	ттаааасааг	GATTAGCA	ТАТСААТТТ	AAAGGCCAC
_			70 11		1190	
		1060	107	10	1080	1090
778106	AAA	ACAGGAC	CGTATAT	TCCCCCC	AGAAACCAG	CGC-CTCCG
	:: TCGTTGCTGCAA			::::: TACTCGAATC		
-				1240		1260
	1100	11	10	1120	1130	1140
778106	TGGCGGC-	CACGCCTC	CGCCCTCC	ACAGCC	TCGGCTCCT	GCTGCTGTG
	:::: GAAATGGTGAAT			:::::		
_	1270					
	1150	1160	1170	1180	1190	
778106	AACTCC-TCTGC	TTCAGCAGAT	'AAGCCATTA'I	CCAACATGAA	GATCCTGACT	
	: :::: : : : ATCTCCATATCC					
_						
120	00 1210	1220	1230	124	0 125	50
	GCTGTCCCGGAA	CAAGGATGAA	GTGAAGGCC-	ATGATTGAG	AAACTCGGG	GGAAGTTG
	::: AGGAG			: :: : PAAAGAATTCT		
_		1380	1390	1400	1410	1420
	1260 1	270 1	.280	1	290	1300
778106	ACGGGGACGG					
	: : :: : CATCTGAGAAAG		: : ATGTTGTTGA		: :: : : AACATGAAG(	
_	1430	1440	1450	1460	1470	1480
		1320				1340
778106	AGGAGGTGGAAA	AGATGAATAA			-AGATGGAG	GAAGTAAAG
778106		AGATGAATAA : : : :	::		-AGATGGAGG	GAAGTAAAG : ::
778106 -	AGGAGGTGGAAA	AGATGAATAA : : : : ATCTTGGTCA	:: \GACTTCTCT	ACACAGAGCTG	-AGATGGAGG: :::::::::::::::::::::::::::::	GAAGTAAAG : ::
-	AGGAGGTGGAAA : : ::::: : ATGCTCTGGATA 1490	AGATGAATAA : : : : ATCTTGGTCA 1500	:: AGACTTCTCT/ 1510	ACACAGAGCTG 1520 1370	-AGATGGAGG : :: : : CCATATTGTGG 1530	GAAGTAAAG : : : GTCATCTAC 1540 1380
-	AGGAGGTGGAAA : : :::::: ATGCTCTGGATA 1490  1 GAAGCC	AGATGAATAA : : : : ATCTTGGTCA 1500  350 1 AACATCCGAG	:: AGACTTCTCTA 1510 .360 I	ACACAGAGCTG 1520 1370 AGGACTT	-AGATGGAG( : :: : : CCATATTGTG( 1530	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG
-	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	:: AGACTTCTCTA 1510  .360 .TTGTGTCTGA .:::::	ACACAGAGCTG 1520 1370 AGGACTT : ::	-AGATGGAG( : :: : : CATATTGTG( 1530 CC' ::	GAAGTAAAG : : : GTCATCTAC 1540  1380 FCCAGGACG : : : :
-	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	:: AGACTTCTCTA 1510  .360 .TTGTGTCTGA .:::::	ACACAGAGCTG 1520 1370 AGGACTT	-AGATGGAG( : :: : : CATATTGTG( 1530 CC' ::	GAAGTAAAG : : : GTCATCTAC 1540  1380 FCCAGGACG : : : :
- 778106 -	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	:: AGACTTCTCTA 1510  .360 .36TTGTGTCTGA .::::: GCTATGGGTGT 1570	ACACAGAGCTG 1520 1370 AGGACTT : :: PGATCCTAACA 1580	-AGATGGAG( ::::::::: CCATATTGTG( 1530 CC' ::: CTTATATCCC' 1590  420	GAAGTAAAG : : : GTCATCTAC 1540  1380 FCCAGGACG : :::: FTCAGGGCT 1600  1430
- 778106 -	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	:: AGACTTCTCTA 1510  .360 .370 .360 .360 .360 .360 .360 .360 .360 .36	ACACAGAGCTG 1520 1370 AGGACTT : : : PGATCCTAACA 1580 1410 1 -CAGGAGTTGT	-AGATGAGG : :: : : : CATATTGTGG 1530 CC :: TTATATCCC 1590  420 TTCTTAGCGC	GAAGTAAAG : : : GTCATCTAC 1540  1380 FCCAGGACG : :::: FTCAGGGCT 1600  1430 ACATCTTGT
- 778106 -	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	:: AGACTTCTCTA 1510  .360 ETTGTGTCTGA :::::: ECTATGGGTGT 1570  ATGAAAATGTA	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : ACAGCAACTCC	-AGATGAGG : :: : : : CATATTGTGG 1530 CC :: CTTATATCCC 1590  420TCTTAGCGC :: : : : CTCCAAGAGGG	GAAGTAAAG : : : GTCATCTAC 1540  1380 FCCAGGACG : : : : FTCAGGGCT 1600  1430 ACATCTTGT : : : GTTATCTCAT
- 778106 -	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	:: AGACTTCTCTA 1510  .360 ETTGTGTCTGA :::::: ECTATGGGTGT 1570  ATGAAAATGTA	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT	-AGATGAGG : :: : : : CATATTGTGG 1530 CC :: CTTATATCCC 1590  420TCTTAGCGC :: : : : CTCCAAGAGGG	GAAGTAAAG : : : GTCATCTAC 1540  1380 FCCAGGACG : : : : FTCAGGGCT 1600  1430 ACATCTTGT : : : GTTATCTCAT
- 778106 - 778106	AGGAGGTGGAAA ::::::: ATGCTCTGGATA 1490  1 GAAGCC :::::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA ::::: TTACTGCTTTAC 1610  1440	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	SECTATEGETE  AGACTTCTCTA  1510  .360 .360 .360 .360 .360 .360 .360 .3	ACACAGAGCTG 1520  1370 AGGACTT : :: PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : ACAGCAACTCC 1640	-AGATGAGG : :: : : : CATATTGTGG 1530 CC' :: ATTATATCCC' 1590  420TCTTAGCGGC :: :: : CTCCAAGAGGGG 1650	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : : : : : FTCAGGGCT 1600  1430 ACATCTTGT : : : : GTATCTCAT 1660  1480
- 778106 - 778106	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC 1610  1440 CCCCTTGGG	AGATGAATAA : : : : ATCTTGGTCA 1500  350	SECTATGGGTGT  TGAAAATGTA  1630  STGAAAATGTA  1630	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : ACAGCAACTCC 1640  1460 G-AAGGCAG	-AGATGAGG : :: : : : CATATTGTGG 1530 CC :: CTTATATCCC 1590  420TCTTAGCGC :: : : : CTCCAAGAGGG 1650  1470 CAGCCTGTTG	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : : : : : FTCAGGGCT 1600  1430 ACATCTTGT : : : : GTATCTCAT 1660  1480 AAGTTGTGG
- 778106 - 778106	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC 1610  1440 CCCCTTGGG : : :: TAGGTAATTCAG	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	SEACAATTGCTC  AGACTTCTCTA  AGACTTCTCTA  AGACTTCTCTA  ATTGTGTGTCTGA  ATTGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : ACAGCAACTCC 1640  1460 G-AAGGCAG : : : : :: GGAAGCTGCAA	-AGATGAGG : :: : : : CATATTGTGG 1530 CC :: CTTATATCCC 1590  420TCTTAGCGC :: : : : CTCCAAGAGGG 1650  1470 GAGCCTGTTG :: : : : AGGCTGGAG	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : ::: : FTCAGGGCT 1600  1430 ACATCTTGT ::: : GTATCTCAT 1660  1480 AAGTTGTGG : : : : ATGTCGAAA
- 778106 - 778106	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC 1610  1440 CCCCTTGGG : : :: TAGGTAATTCAG	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	SEACAATTGCTC  AGACTTCTCTA  AGACTTCTCTA  AGACTTCTCTA  ATTGTGTGTCTGA  ATTGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : : ACAGCAACTCC 1640  1460 G-AAGGCAG	-AGATGAGG : :: : : : CATATTGTGG 1530 CC :: CTTATATCCC 1590  420TCTTAGCGC :: : : : CTCCAAGAGGG 1650  1470 GAGCCTGTTG :: : : : AGGCTGGAG	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : ::: : FTCAGGGCT 1600  1430 ACATCTTGT ::: : GTATCTCAT 1660  1480 AAGTTGTGG : : : : ATGTCGAAA
- 778106 - 778106 - 778106	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC 1610  1440 CCCCTTGGG : : :: TAGGTAATTCAG 1670	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	SEACAATTGCTC  AGACTTCTCTA  1510  360  STTGTGTGTCTGA  SCTATGGGTGT  1570  CT  CATGAAAATGTA  1630  CGACAATTGCTC  1690  1500	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : ACAGCAACTCC 1640  1460 G-AAGGCAG : :: : :: EGGAAGCTGCAA 1700  1510	-AGATGAGG : :: : : : CATATTGTGG 1530 CC :: CTTATATCCC 1590  420CTTAGCGC :: :: : CTCCAAGAGGG 1650  1470 GAGCCTGTTG :: :: : AGGCTGGAGG 1710  1520	GAAGTAAAG : : : GTCATCTAC 1540  1380 FCCAGGACG : :::: FTCAGGGCT 1600  1430 ACATCTTGT :::: GTATCTCAT 1660  1480 AAGTTGTGG : ::: ATGTCGAAA 1720
- 778106 - 778106 - 778106	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC 1610  1440 CCCCTTGGG : : :: TAGGTAATTCAG 1670  1 CCCCAAGA	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	SEACAATTGCTC  AGACTTCTCTA  AGACTTCTCTA  AGACTTCTCTA  ATTGTGTGTCTGA  ATTGTGTGTCTGA  ATTGTGTGTCTGA  ATTGTGTGTCTGA  ATTGTGTGTCTGA  ATTGTGTGTGTGTGA  ATTGTGTGTGTGTA  ATTGTGTGTG	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : ACAGCAACTCC 1640  1460 G-AAGGCAG : :: : :: EGGAAGCTGCAA 1700  1510	-AGATGAGG : :: : : : CATATTGTGG 1530 CC' :: CTTATATCCC' 1590  420TCTTAGCGC' :: :: : CTCCAAGAGGG 1650  1470CAGCCTGTTGG' :: :: : AGGCTGGAGG' 1710  1520 AAAAAGC-AA	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : : : : : FTCAGGGCT 1600  1430 ACATCTTGT : : : : GTATCTCAT 1660  1480 AAGTTGTGG : : : : ATGTCGAAA 1720  AGGGC
- 778106 - 778106 - 778106	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC 1610  1440 CCCCTTGGG : : : TAGGTAATTCAG 1670  1 CCCCAAGA : ::: CTGTAAAAAAAAC	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	GACAATTGCTC  AGACTTCTCTA  AGACTTCTCTA  AGACTTCTCTA  AGACTTCTCTA  ATGGGGGTGT  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGCTC  ATGACAATTGCTC  AGACAATTGCTC  AGACAATTCC  AGACAATTC	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410      1 -CAGGAGTTGT ::: : : ACAGCAACTCC 1640  1460 G-AAGGCAG : : : : :: EGAAGCTGCAA 1700  1510 GCGCTCTCCAA : : : : : ETCAACTGCAG	-AGATGAGG : :: : : : CATATTGTGG 1530 CC' :: ATTATATCCC' 1590  420CTTAGCGGG :: :: : CTCCAAGAGGG 1650  1470CAGCCTGTTGG :: :: : AGGCTGGAGG 1710  1520 AAAAAAGC-AGGCAGAGACATTGAGAGACATTGAGAGACATTGAGAGAGA	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : ::: : FTCAGGGCT 1600  1430 ACATCTTGT ::: : GTATCTCAT 1660  1480 AAGTTGTGG : :: : ATGTCGAAA 1720  AGGGC :::: : AGGGCGTCA
- 778106 - 778106 - 778106	AGGAGGTGGAAA : : ::::: ATGCTCTGGATA 1490  1 GAAGCC :: ::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA : :::: TTACTGCTTTAC 1610  1440 CCCCTTGGG : : : TAGGTAATTCAG 1670  1 CCCCAAGA : ::: CTGTAAAAAAAAC	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	GACAATTGCTC  AGACTTCTCTA  AGACTTCTCTA  AGACTTCTCTA  AGACTTCTCTA  ATGGGGGTGT  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGTA  ATGAAAATGCTC  ATGACAATTGCTC  AGACAATTGCTC  AGACAATTCC  AGACAATTC	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410 1 -CAGGAGTTGT ::: : : ACAGCAACTCC 1640  1460 G-AAGGCAG : : : : :: GGAAGCTGCAA 1700  1510 GCGCTCTCCAA	-AGATGAGG : :: : : : CATATTGTGG 1530 CC' :: ATTATATCCC' 1590  420CTTAGCGGG :: :: : CTCCAAGAGGG 1650  1470CAGCCTGTTGG :: :: : AGGCTGGAGG 1710  1520 AAAAAAGC-AGGCAGAGACATTGAGAGACATTGAGAGACATTGAGAGAGA	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : ::: : FTCAGGGCT 1600  1430 ACATCTTGT ::: : GTATCTCAT 1660  1480 AAGTTGTGG : :: : ATGTCGAAA 1720  AGGGC :::: : AGGGCGTCA
- 778106 - 778106 - 778106 - 778106	AGGAGGTGGAAA ::::::: ATGCTCTGGATA 1490  1 GAAGCC :::::: AAACCTGCCGCC 1550  1390 TCTCCGCCTCCA ::::: TTACTGCTTTAC 1610  1440 CCCCTTGGG :::: TAGGTAATTCAG 1670  1 CCCCAAGA:::: CTGTAAAAAAAC 1730	AGATGAATAA : : : : : ATCTTGGTCA 1500  350	:: AGACTTCTCTA 1510  .360 .::::::: CTTGTGTCTGA .:::::: CTATGGGTGT .570  ATGAAAATGTA .630  GACAATTGCTC .690 1500 TCAGGGGCTC .::::::: CTCAGAGGCTC 1750 540	ACACAGAGCTG 1520  1370 AGGACTT : : : PGATCCTAACA 1580  1410      1 -CAGGAGTTGT ::: : : ACAGCAACTCC 1640  1460 G-AAGGCAG : : : : :: GGAAGCTGCAA 1700  1510 GCGCTCTCCAA : : : : : GTCAACTGCAG 1760	-AGATGAGG : :: : : : CATATTGTGG 1530	GAAGTAAAG : : : : GTCATCTAC 1540  1380 FCCAGGACG : :::: : FTCAGGGCT 1600  1430 ACATCTTGT ::: : GTATCTCAT 1660  1480 AAGTTGTGG : :: : ATGTCGAAA 1720  AGGGC ::::: AGGGCGTCA 1780

-	GTCTACAC	CACTTCATTT'	TGCAGCTGGG		G-TGTCCGTG	: :: ::: : GTGGAAT-AT 1830
778106	CTCTTAAAC	GGA-GGAGCA	GCTGTGGATC		TGGACTG	620 GAACACTCTGC-
_	CTGCTACAC	GCATGGAGCT	GATGTGCATG		AGGAGGCCTT	: :: :: ::: GTAC-CTTTGCA 1890
778106	GCAT		AGAAA	AGGTGG-GAAG		1660 CAGT
_		GTTCTTATGG	ACATTATGA	AGTTGCAGAAC 1930	TTCTTGTTAA	:::: ACATGGAGCAGT 1950
778106	-GCCACCCT	TTGGCCTG	GTGGACAT		AGGAACCAAC	TCCTAC
_		PAGCTGATTT.	ATGGAAATTI	: ::: FACACCTTTAC 1990	ATGAAGCAGC	AGCAAAAGGAAA
778106		TACAAGCT	GCAGCTTC		CGAC-AA	GGAAAACAGGTA
	ATATGAAA1 2020	TTTGCAAACT	TCTGCTCCAC		ACCCTACCAA	::::::::: AAAAAACAGGGA 2070
		TTCAGG	TCCTGGGGC		CGGT	-GATCGGTAG
-	TGGAAATA	CTCCTTTGGA	TCTTGTTAAA	: :: :: AGATGGAGATA 2110	CAGATATTCA	AGATCTGCTTAG 2130
778106	CAACA		AGATGCCGT	CCAAGGAGGAT		TTGAGCA
_	GGGAGATG	CAGCTTTGCT	AGATGCTG-C	CCAAGAAGGGT 2170	TGTTTAGCCA	GAGTGAAGAAGT
778106				ATAT	-GAAGAAA	1870 -AAACCGGGAAC
			TAAATTGCCC	::: GCGATACCCAA 2230	GGCAGACATT	CAACACCTTTAC
778106		CTCCA	AAAATTTCAC		AAAAAGTTCT	ACCCCCTGGAGA
	:: ::: ATTTAGCAG 2260	GCTGGTTATA	ATAATTTA		AGTATTTGTT	ACAACACGGAGC 2310
778106	1930 TTGACTA		TGAAG		1950	AG
_	: :: TGATGTGA	::: ::: :: ATGCCCAAGA	::: CAAAGGAGGA		: :: TACATAATGO	:: AGCATCTTACGG
778106		1960 -TGAAGAAGC				1990 CCAAGTCCAA
-	GCATGTAG	:: :: :::	: TCTACTAATA	: :::: ::: AAAGTATAATG	: :::: CATGTGTCAA	::: : ::: TGCCACGGACAA
		2000	2010	2020		2020

778106	GCTCCCC	AAGCCAGTTC	AGGAC-CTC	ATCAAGATG-	AT	CTTTGA
		: :: ::				
-	ATGGGCTTTC- 2440			2470		2490
	2040				2060	
778106	TGTGGAAAGT-				TGGTGGAGTA : ::: :	
-	::: : :: TGTTGCTAGCC 2500			гтааааатса	GGAAGGACAA	ACACCTTTAG
778106	2080 ATCGACCTTCA			2100 TTGGGGAAGC		GCAGATC
	:: ::::					
-	ATTTAGTTTCA 2560		2580	2590	2600	2610
	2120 21 -CAGGCCGCAT	ACTCCA	TCCT	CAGTGAGGTC		TGTCTCAGGG
_	TCTGCCCTCTT	: :: GTTACAAGCC				
_	2620	2630	2640	2650	266	0
	170 21 CAGCAGCGA-C					
	::: :: :: :: :: :: :: :: :: :: :: :: ::					
- 26	70 2680					
778106	2230 ACGACTTT	GGGATG	40 AAGAAGC	CTCCGCTCCT		2260 -GAACAA
	:: :::: :	::::	:::: :	::::::::	m » cmmc » » cm	:::::
- 27	ACAACTTATCT 30 2740	'GGGAGTTTTT	CAGAACTGT	CTTCAGTAGT	TAGTTCAAGT	
	ACAACTTATCT 30 2740 2270	GGGAGTTTTT 2750 2280	CAGAACTGT 276	CTTCAGTAGT 0 277	TAGTTCAAGT 0 278	2290
	ACAACTTATCT 30 2740 2270 -TGCAGACAGT	GGGAGTTTTT 2750 2280 GTGCAGGCCA	CAGAACTGT 276 AGGCGGA	CTTCAGTAGT 0 277	TAGTTCAAGT 0 278	2290
	ACAACTTATCT 30 2740 2270 -TGCAGACAGT	GGGAGTTTTT 2750 2280 GTGCAGGCCA ::::::	CAGAACTGT 276 AGGCGGA	CTTCAGTAGT 0 277	TAGTTCAAGT 0 278	0 2290 AATGC- :::::
778106	ACAACTTATCT 30 2740  2270  TGCAGACAGT :::::::: GTGCTTCCAGT	GGGAGTTTTT 2750 2280 GTGCAGGCCA ::::::	AGGCGGA AGGAGGTTC	CTTCAGTAGT 0 277 CAGGAGTAGA	TAGTTCAAGT 0 278 TTTTAGCATA	2290 AATGC- :::: ACTCAATTCG
778106 - 27	ACAACTTATCT 30 2740  2270  TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800	2750 2750 2280 CGTGCAGGCCA :: :: : CTTGGAGAAAA 2810	CAGAACTGT 276  AGGCGGA ::: :: AGGAGGTTC 282 0 23	CTTCAGTAGT 0 277 CAGGAGTAGA 0 283	TAGTTCAAGT 0 278 TTTTAGCATA 0 284 320 2	0 2290 AATGC- :::: ACTCAATTCG 0
778106 - 27	ACAACTTATCT 30 2740  2270  TGCAGACAGT :::::::: GTGCTTCCAGT	2280 2280 CGTGCAGGCCA ::::: CTTGGAGAAAA 2810 230TTGACA	CAGAACTGT 276  AGGCGGA :::::: AGGAGGTTC 282  0 23 ACCTGCTGG	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283 10 2 ACATCGAGGT	TAGTTCAAGT 0 278 TTTTAGCATA 0 284 320 2	0 2290 AATGC- :::: ACTCAATTCG 0
778106 - 27	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800	2280 2280 CGTGCAGGCCA ::::: CTTGGAGAAAA 2810 230TTGACA	CAGAACTGT 276  AGGCGGA :::::: AGGAGGTTC 282  0 23 ACCTGCTGG. ::::::::	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283 10 2 ACATCGAGGT : :: :	TAGTTCAAGT 0 278  TTTTAGCATA 0 284  320 2 G-GCCTACAG : : ::::	2290 AATGC- :::: ACTCAATTCG 0 330 TCTGCTCAGG :::::
778106 - 27 778106	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800	2280 2280 CGTGCAGGCCA ::::: CTTGGAGAAAA 2810 230TTGACA ::::	CAGAACTGT 276  AGGCGGA ::: :: AGGAGGTTC 282  0 23 ACCTGCTGG :::: ::: ACCTAATGG	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283 10 2 ACATCGAGGT : :: : ATATATTTGA	TAGTTCAAGT 0 278  TTTTAGCATA 0 284  320 2 G-GCCTACAG : : ::::	2290AATGC- :::: ACTCAATTCG 0 330TCTGCTCAGG :::: ATCACTTTGG
778106 - 27 778106 - 28	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800  TAAGGAATCTT 50 2860	2280 2280 CGTGCAGGCCA ::::: CTTGGAGAAAA 2810 230TTGACA :::: CGGACTTGAGC	CAGAACTGT 276  AGGCGGA ::: :: AGGAGGTTC 282  0 23 ACCTGCTGG :::: ::: ACCTAATGG 288	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : :: ATATATTTGA 0 289	TAGTTCAAGT 0 278  TTTTAGCATA 0 284  320 2 G-GCCTACAG : : :::: GAGAGAACAG 0 290	2290AATGC- :::: ACTCAATTCG 0 330TCTGCTCAGG :::: ATCACTTTGG
778106 - 27 778106 - 28	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800  TAAGGAATCTT 50 2860  2340 23	2280 2280 CGTGCAGGCCA ::::: CTTGGAGAAAA 2810 230TTGACA :::: CGGACTTGAGC 2870	CAGAACTGT 276  AGGCGGA ::: :: AGGAGGTTC 282  0 23 ACCTGCTGG. ::: ::: ACCTAATGG. 288	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283 10 2 ACATCGAGGT : :: : ATATATTTGA 0 289	TAGTTCAAGT 0 278  TTTTAGCATA 0 284  320 2 G-GCCTACAG : :::: GAGAGAACAG 0 290	2290AATGC- :::: ACTCAATTCG 0 330TCTGCTCAGG :::: ATCACTTTGG 0
778106 - 27 778106 - 28	ACAACTTATCT 30 2740 2270 -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800 TAAGGAATCTT 50 2860 2340 23 GGAGGGTCTGA	2280 2280 CGTGCAGGCCA ::::: CTTGGAGAAAA 2810 230TTGACA :::: CGGACTTGAGC 2870	CAGAACTGT 276  AGGCGGA ::: :: AGGAGGTTC 282  0 23 ACCTGCTGG :::: ::: ACCTAATGG 288  2360 CAGCAAGGA	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283 10 2 ACATCGAGGT : :: : ATATATTTGA 0 289 2370 ICCCATCGA-	TAGTTCAAGT 0 278  TTTTAGCATA 0 284  320 2 G-GCCTACAG : : :::: GAGAGAACAG 0 290 TGTCA	2290AATGC- :::: ACTCAATTCG 0 330TATGC- :::: ATCACTTTGG 0 2380 ACTATG-
778106 - 27 778106 - 28 . 778106	ACAACTTATCT 30 2740 2270 -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800 TAAGGAATCTT 50 2860 2340 23 GGAGGGTCTGA	2280 2280 2280 230 2310 2310 230TTGACA :::: CGGACTTGACA :::: CGGACTTGAGC 2870 250 250 CTGATAG ::::: CTGAGATAGGGG	CAGAACTGT 276  AGGCGGA ::: :: AGGAGGTTC 282  0 23 ACCTGCTGG ::: ::: ACCTAATGG 288  2360 CAGCAAGGA :: ::::: CA-CAAGGA	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : :: : ATATATTTGA 0 289  2370 ICCCATCGA- : :: :	TAGTTCAAGT 0 278  TTTTAGCATA 0 284  320 2 G-GCCTACAG : :::: GAGAGAACAG 0 290 TGTCA :: ::: ATTGGAATCA	2290AATGC- :::: ACTCAATTCG 0 330TATGG- :::: ATCACTTTGG 0 2380 ACTATG- :::::
778106 - 27 778106 - 28 778106 - 29	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800   TAAGGAATCTT 50 2860  2340 23 GGAGGGTCTGA ::: AT-GTATTAGT 10 292	2280 2280 2280 230 2310 2310 230TTGGAAAAA 2310 230TTGACA 2370 250 2870 250 27GAATAG 2111 2400	CAGAACTGT 276  AGGCGGA ::: :: AGGAGGTTC 282  0 23 ACCTGCTGG ::: ::: ACCTAATGG 288  2360 CAGCAAGGA :: ::::: CA-CAAGGA 0 2	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : : : ATATATTTGA 0 289  2370 ICCCATCGA- : : : GCTGAAGGAG 940 2	TAGTTCAAGT 0 278  TTTTAGCATA 0 284  320 2 G-GCCTACAG : :::: GAGAGAACAG 0 290 TGTCA :: ::: ATTGGAATCA 950 2	2290AATGC- :::: ACTCAATTCG 0 330 -TCTGCTCAGG :::: ATCACTTTGG 0 2380 ACTATG- :::: ATGCTTATGG 960
778106 - 27 778106 - 28 778106 - 29	ACAACTTATCT 30 2740 2270 -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800  TAAGGAATCTT 50 2860 2340 23 GGAGGGTCTGA ::: : AT-GTATTAGT 10 292 2390 -AGAAGCTCA ::::::	2280 2280 2280 230 2310 2310 2310 2310 2310 2310 2310	CAGAACTGT 276  AGGCGGA :::::: AGGAGGTTC 282  0 23 ACCTGCTGG ::::::: ACCTAATGG 288  2360 CAGCAAGGA ::::::: CA-CAAGGA 0 2 2410 TAAGGTGGT ::::::::	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : : : : ATATATTTGA 0 289  CCCCATCGA- : : : : GCTGAAGGAG 940 2  2420  IGACAGAGAGAT : : : : :	TAGTTCAAGT 0 278 TTTTAGCATA 0 284 320 2 G-GCCTACAG : : :::: GAGAGAACAG 0 290TGTCA :: ::: ATTGGAATCA 950 2 2430TCTGAAGAA ::: ::	2290AATGC- :::: ACTCAATTCG 0 330 -TCTGCTCAGG :::: ATCACTTTGG 0 2380 ACTATG- :::: ATGCTTATGG 960 2440 GCCGAGATCA :::::
778106 - 27 778106 - 28 778106 - 29 778106	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800   TAAGGAATCTT 50 2860  2340 23 GGAGGGTCTGA ::: : AT-GTATTAGT 10 292  2390 AGAAGCTCA :::::: ACATAGGCACA	2280 2280 2280 230 2310 2310 2310 2310 2310 2310 2310	CAGAACTGT 276  AGGCGGA :::::: AGGAGGTTC 282  0 23 ACCTGCTGG ::::::: ACCTAATGG 288  2360 CAGCAAGGA ::::::: CA-CAAGGA 0 2 2410 TAAGGTGGT ::::::::	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : : : : ATATATTTGA 0 289  CCCCATCGA- : : : : GCTGAAGGAG 940 2  2420  IGACAGAGAGAT : : : : :	TAGTTCAAGT 0 278 TTTTAGCATA 0 284 320 2 G-GCCTACAG : : :::: GAGAGAACAG 0 290TGTCA :: ::: ATTGGAATCA 950 2	2290AATGC- :::: ACTCAATTCG 0 330 -TCTGCTCAGG :::: ATCACTTTGG 0 2380 ACTATG- :::: ATGCTTATGG 960 2440 GCCGAGATCA :::::
778106 - 27 778106 - 28 778106 - 29 778106 -	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800   TAAGGAATCTT 50 2860  2340 23 GGAGGGTCTGA ::: :: AT-GTATTAGT 10 292  2390 AGAAGCTCA :::::: ACATAGGCACA 2970 29	2280 2280 2280 230 2310 2310 2310 2310 2310 2310 2310	CAGAACTGT 276  AGGCGGA :::::: AGGAGGTTC 282  0 23 ACCTGCTGG. ::::::: ACCTAATGG. 288  2360 CAGCAAGGA :::::::: CA-CAAGGA 0 2 2410 TAAGGTGGT ::::::: TAAAGGAGT 2990 460	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : : : ATATATTTGA 0 289  2370 ICCCATCGA- : : :: GCTGAAGGAG 940 2 2420 IGACAGAGAGT : : : : CGAGAGAGACTT 3000  2470	TAGTTCAAGT 0 278	2290AATGC- :::: ACTCAATTCG 0  330TATGC- :::: ATCACTTTGG 0  2380 ACTATG- :::: ATGCTTATGG 960  2440 GCCGAGATCA :::: CACAAGGTCT 3020
778106 - 27 778106 - 28 778106 - 29 778106 -	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800   TAAGGAATCTT 50 2860  2340 23 GGAGGGTCTGA ::: : AT-GTATTAGT 10 292  2390 AGAAGCTCA :::::: ACATAGGCACA 2970 29  TCAGGAAGTAT	2280 2280 2280 230 2310 2310 2310 2310 2310 2310 2310	CAGAACTGT 276  AGGCGGA :::::: AGGAGGTTC 282  0 23 ACCTGCTGG ::::::: ACCTAATGG 288  2360 CAGCAAGGA ::::::: CA-CAAGGA 0 2  2410 TAAGGTGGT :::::: TAAAGGAGT 2990  460 AACAC	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : : : ATATATTTGA 0 289  CCCCATCGA- : : :: GCTGAAGGAG 940 2  1GACAGAGAGAT : : : : CGAGAGAGAT  CGAGAGAGAT  3000  2470  -TCATGCAA	TAGTTCAAGT 0 278 TTTTAGCATA 0 284 320 2 G-GCCTACAG : : :::: GAGAGAACAG 0 290TGTCA :: ::: ATTGGAATCA 950 2 2430 -TCTGAAGAA ::: :: ATCTCCGGAC 3010 CCACAC	2290AATGC- :::: ACTCAATTCG 0  330TATGC- :::: ATCACTTTGG 0  2380 ACTATG- :::: ATGCTTATGG 960  2440 GCCGAGATCA :::: CACAAGGTCT 3020
778106 - 27 778106 - 28 778106 - 29 778106 -	ACAACTTATCT 30 2740  2270  -TGCAGACAGT ::: :::: GTGCTTCCAGT 90 2800   TAAGGAATCTT 50 2860  2340 23 GGAGGGTCTGA ::: :: AT-GTATTAGT 10 292  2390 AGAAGCTCA :::::: ACATAGGCACA 2970 29	2280 2280 2280 230 2310 2310 2310 2310 2310 2310 2310	CAGAACTGT 276  AGGCGGA :::::: AGGAGGTTC 282  0 23 ACCTGCTGG ::::::: ACCTAATGG 288  2360 CAGCAAGGA ::::::: CA-CAAGGA 0 2  410 TAAGGTGGT :::::: TAAAGGAGT 2990  460 AACAC :::::	CTTCAGTAGT 0 277  CAGGAGTAGA 0 283  10 2 ACATCGAGGT : : : ATATATTTGA 0 289  CCCCATCGA- : : :: GCTGAAGGAG 940 2  1GACAGAGAGAT : : : : CGAGAGAGAT : : : : CGAGAGACTT 3000  2470TCATGCAA : : : :	TAGTTCAAGT 0 278 TTTTAGCATA 0 284 320 2 G-GCCTACAG : : :::: GAGAGAACAG 0 290TGTCA :: ::: ATTGGAATCA 950 2 -TCTGAAGAA ::: :: ATCTCCGGAC 3010 CCACAC : : :	2290AATGC- :::: ACTCAATTCG 0 330 TCTGCTCAGG :::: ATCACTTTGG 0 2380 ACTATG- :::: ATGCTTATGG 960 2440 GCCGAGATCA :::: AACAAGGTCT 3020

TOTAL   TOTA	770106	2480	2490			2510
2500   2530   2540   2550   2560   2570   2580   2580   2580   2580   2580   2580   2580   2580   2580   2580   3150   3160   3170   3180   3190   3200   3150   3160   3170   3180   3190   3200   3200   3200   2560   2570   2580   2590   2580   2590   2580	778106					
778106 TAAGATAGAG—CCTCAAGGCCAA—TGCCAGGGTTACAAGCC—CT——TTAAGCAG	_					
	778106					-TTAAGCAG
2560   2570   2580   2590		:::: ::: ::	: ::: : :	: : :::::	::	:: :: ::
778106 CTTCATAACCGAAGATTGCTGTGCACGGGTCCAGGA	_					
### CTTTGTAACAAGAAA-CTATGGGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGAA 3210 3220 3230 3240 3250  2600 2610 2620 2630  778106CCACCAACTTGCTGGGATCCTGTCCCA-GGGTCTTCGGA		CTTCATAACCGAAGA	TTGCTGTGGCACGG	GTCCAGG	A	
					-	GTTTCTGAA
778106CCACCAACTTTGCTGGGATCCTGTCCCA-GGGTCTTCGGA						
	778106					G <u>D</u>
3260   3270   3280   3290   3300   3310	770100					
778106TAGCCCCGCCTGAAGCGCCCGTGACAGGCTACATGTTTGGTAAAGG	- 32					
### HATTATCCACAAAAGGCTTTGATGAAAAGGCATGCTTACATAGGTGGTATGTTTGGAGCTGG ### 3320		2010		•		
AATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGCTGG 3320 3330 3340 3350 3360 3370  2690 2700 2710 2720 2730 2740  778106 GATCTATTTGCTGACAATGGTCTCCAAGAGTGCCAACTACTGCCATACGTCTCAGGGAGA :::::::::::::::::::::::::::::::	//8106					
T18106   GATCTATTTCGCTGACATGGTCTCCAAGAGTGCCAACTACCTCCCATACGTCTCAGGGAGA	- 3	AATTATCCACAAAGG	CTTTGATGAAAGGC	ATGCGTACATAGG	TGGTATGTT	TGGAGCTGG
	770106					
3380   3390   3400   3410   3420   3430   3430	778106					
778106 CCCAATAGGCTTAATCCTGTTGGGAGAAGTTGCCCTTGGAAACATGTATG	- 3					
		2750	2760	2770	2780	2790
	778106					
2800 2810 2820 2830 2840  778106 AACTGAAGCACGCTTCACATATCAGCAAGT—TACC—CA——AGGGCAAGCACAGTGT  :: :: :: :: :: :: :: :: :: :: :: :: ::	_					
778106 AACTGAAGCACGCTTCACATATCAGCAAGT—TACC—CA——AGGGCAAGCACAGTGT  :: :: :: :: :: :: :: :: :: :: :: :: ::	_	3440 34	50 3460	3470	3480	3490
_ CTCTTTTGC-CGGGTAACCT-TGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAATGG	778106					
3500   3510   3520   3530   3540   3550		:: :: :: :	. : : : : : : : : : : : : : : : : : : :	: :::::	:: ::::	: : ::
778106 CAAAGGTTTGGGCAAAACTACCCCTGATCCTTCAGCTAAC  :::::::::::::::::::::::::::::::::	_					
_ CACATTCTCCTCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAAATGGCCTAGC 3560 3570 3580 3590 3600  2890 2900 2910 2920 2930 2940  778106 ATTAGTCTGGATGGTGTAGACGTTCCTCTTGGGACCGGGATTTCATCTGGTGTGAATGAC ::::::::::::::::::::::::::::::::::::	778106	CAAAGGTTTC	GGCAAAACTACC	CCTGATCCTT		CTAAC
3560 3570 3580 3590 3600						
778106 ATTAGTCTGGATGGTGTAGACGTTCCTCTTGGGACCGGGATTTCATCTGGTGTGAATGAC  :::::::::::::::::::::::::::::::::::	_					
ATTAG-CTGAATATGTTATTTACAGAGGAGAACAGGCTTATCCTGAGTATTTAAT 3610		CACATTCTCCTCCAC 3560	GTCATCACTCAGTC 3570 3580	ACTGGTAGGCC 3590	CAGTGTAAA 3600	TGGCCTAGC
3610 3620 3630 3640 3650 3660  2950 2960 2970 2980 2990  778106 ACCTCTCTACTATATAACGAGTACATTGTCTATGATATTGCTCAGGTAAA :: ::::::::::::::::::::::::::::::::		CACATTCTCCTCCAC 3560 2890 29 ATTAGTCTGGATGGT	GGTCATCACTCAGTC 3570 3580 000 2910 GTAGACGTTCCTCT	ACTGGTAGGCC 3590 2920 TGGGACCGGGATT	CAGTGTAAA 3600 2930 TCATCTGGT	TGGCCTAGC 2940 GTGAATGAC
778106 ACCTCTACTATATAACGAGTACATTGTCTATGATATTGCTCAGGTAAA :: ::::::::::::::::::::::::::::::::		CACATTCTCCTCCAC 3560  2890 29 ATTAGTCTGGATGGT	GGTCATCACTCAGTC 3570 3580 000 2910 CGTAGACGTTCCTCT :: :: :	ACTGGTAGGCC 3590 2920 TGGGACCGGGATT	CAGTGTAAA 3600 2930 TCATCTGGT	2940 GTGAATGAC
:: :::::::::::::::::::::::::::::::::::	_	CACATTCTCCTCCAC 3560  2890 29 ATTAGTCTGGATGGT :::::::::::::::::::::::::::::::	GTCATCACTCAGTC 3570 3580 000 2910 CGTAGACGTTCCTCT :: :: : GTTATTTACAGA	ACTGGTAGGCC 3590 2920 TGGGACCGGGATT : :: :: :: GGAGAACAGGCTT	CAGTGTAAA 3600 2930 TCATCTGGT :::::	2940 GTGAATGAC :: ::
<del>-</del>	_ 36	2890 29 ATTAGTCTGGATGGT ::::::::::: ATTAG-CTGAATATC 10 3620 2950 29	GTCATCACTCAGTC 3570 3580  000 2910  GTAGACGTTCCTCT :: :: : GTTATTTACAGA 3630	ACTGGTAGGCC 3590  2920 TGGGACCGGGATT :::::::: GGAGAACAGGCTT 3640  2970	CAGTGTAAA 3600 2930 TCATCTGGT :::::ATCCTGA 3650 2980	2940 GTGAATGAC :: :: GTATTTAAT 3660 2990
	_ 36	CACATTCTCCTCCAC 3560  2890 29 ATTAGTCTGGATGGT :::::::::: ATTAG-CTGAATATC 10 3620  2950 2950 2950 ACCTCTCTACTATATC	GTCATCACTCAGTC 3570 3580  000 2910  GTAGACGTTCCTCT :: :: : GTTATTTACAGA 3630  060  CAACGAGTAC	ACTGGTAGGCC 3590  2920 TGGGACCGGGATT : :: :: :: GGAGAACAGGCTT 3640  2970ATTGTCTATG-	CAGTGTAAA 3600 2930 TCATCTGGT ::::ATCCTGA 3650 2980ATATTGC	2940 GTGAATGAC :: :: GTATTTAAT 3660 2990 CTCAGGTAAA

```
3010
                     3020
778106 TCTGAAGTA--TCTGCTGAAACTGAAAT--TCAA-----TTTTAAG
      :: :: :: ::::: :::: ::::
    A---AACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTGGCCTCTACGTTTTACT
          3730 3740 3750 3760 3770
        3040
778106 ACCTCCCTGTGGTAA----
    ::::::::::
    CCTTTGCTGAAAAAAAAAA
   3780 3790
>_ PARP-1
                                 3045 nt vs.
> SEQ ID NO:2
                                 3816 nt
scoring matrix: , gap penalties: -12/-2
46.3% identity; Global alignment score: -435
         10
                    20 30
                                 40
CGCGCTGCTCCGCCGCGCGGGGCAGCCGGGGGGGCAGGGAGCCCAGCGAGGGGCGCGCG
         10 20 30 40 50
                           70
     50
        60
649550 --GGCGCGCCTCTTGCAA-------GA------AATGCAGCGAG---AGCATCCC---
:::::: : : : : : : : : : :::
    TGGGCGCGCCCATGGGACTGCGCCGGATCCGGTGACAGCAGGGAGCCAAGCGGCCCGGG
            80 90 100 110 120
                           110 120
      90
              100
649550 -CAAGGACTCG----CTCCGGATGGCCA-----TCATGGTGCAGTCGCCCATGT
    CCCTGAGCGCGTCTTCTCCGGGGGGCCTCGCCCTCCTGCTCGCGGGGCCGGGGCTCCTGC
        130
            140 150 160 170
            140
                  150
                                160
649550 T----TGATGGAAAAGTCCCACACTG-----GTACCACTTCTCCT-GCTTCT
    {\tt TCCGGTTGCTGGCGTTGCTGGCTGTGGCGGCGGCCAGGATCATGTCGGGTCGCCGCT}
        190
              200 210 220 230
              190
                        200
                              210
649550 G-GAAGGTGGGCCA-CTCCATCCG---GCACC-CTGACGTTGAGGTGGATGGGTTCTCT-
    GCGCCGGCGGGGAGCGCCTGCGCGAGCGCCGAGGCCGTGGAGCCGGCCCCC
         250
             260 270 280 290 300
       230
             240
                           250
                                 260
649550 --GAGCT-TCGGTGGGATGATCAGCA-----GAA--AGTCAAGAAGACAGCGGA
     GAGAGCTGTTCGAGGCGTG--CCGCAACGGGGACGTGGAACGAGTCAAGAGG-CTGGTGA
             320 330 340
         310
         280
                  290
649550 AGCTGGAGGAG-TGA-CAG--GCAAA-----GGCCAGGA------TGGAATTGG
    CGCCTGAGAAGGTGAACAGCCGCGACACGGCGGGCAGGAAATCCACCCCGCTGCACTTCG
    360
                380
                      390
              320
                     330
   310
                            340
                                   350
649550 TAGCAAG-----GCAGAGAAGACTCTGGGTGACT--TTGCAGCAGAGTA-TGCCAA-GT
```

_	CCGCAGG 420	STTTTGGGCG 430	GA-AAGACG- 440	FAGTTGAATAT 450	TTGCTTCAGAA1 460	rggtgcaaatgt 470
	CCAACAG		CAAGGGG-	TGTATGGAG	400 AAGATAGAAAAC :::	410 GGGCCAGGTGCĠ
_					TTCATAATGCAT	rgctcttttggt 20 530
649550		AAGAAGA		G-GACCCGGAG.	450 AAGCCACAO :: :: ::	SCTAGGCATGAT
-	CATGCTG			GCGACATGGTG	CAGACCCCAATO	GCTCGAGATAAT 30 590
649550	TG-ACCG				CAGGGAGGAGCT	LO 520 PGGGTTTCCGGC ::::::
-	TGGAATT	ATACTCCTC 600	TCCATGAAGC 610	TGCAATTA 620		GATGTTTGC 640
649550	:	:::: :	TCAGCTCAAG		:::	TACAGAGGATAA
	A	ATTGTGCT-G 650		GAGCTGAGCCA 670		FACAGATGG-AA 690
649550			-	AGG	610 AGTCAAGAGTG <i>i</i> ::: ::	AAGGAAAGAGAA
_	GGACAGO 700	CATTGGATTT 710	AGCAGATCCA 720	TCTGCCAAAGC. 730	AGTGCTTACTG( 740	GTGAATATAAGA 750
649550	630 AAGGCGA	TGAGGTGGA	TGGAGTGGAT	660 GAAGTGGCGAA : ::::::		670 TCTAAA ::::
649550 	AAGGCGA	ATGAGGTGGA : :: AACTCTTAGA 770	TGGAGTGGAT :::: AAGTGCCA 780	GAAGTGGCGAA : :::::: : GGAGTGGCAAT 790	:::::: GAAGAAAAAATO 800	
-	AAGGCGA ::: :: AAGATGA 760	ATGAGGTGGA : :: ACTCTTAGA 770 580 AGAAAAAAGAC	TGGAGTGGAT :::: AAGTGCCA 780	GAAGTGGCGAA : :::::: : GGAGTGGCAAT 790 700 TAAGCTTGAAA	:::::: GAAGAAAAAATC 800 710	TCTAAA :::: GATGGCTCTACT 810 720 GCTCAGAACGAC
-	AAGGCGA ::: :: AAGATGA 760  6 AAA	ATGAGGTGGA : :: ACTCTTAGA 770 580 AGAAAAAGAC ::: : :	TGGAGTGGAT :::: AAGTGCCA 780 690 CAAGGATAG :::::	GAAGTGGCGAA : :::::: GGAGTGGCAAT 790  700 TAAGCTTGAAA ::: :::	:::::: GAAGAAAAAAT 800 710 AAGCCCTAAAG ::::::	TCTAAA :::: GATGGCTCTACT 810 720 GCTCAGAACGAC
 649550  7	AAGGCGA ::: :: AAGATGA 760  6 AAA : : CACACCA 820  30 CTGATCI	ATGAGGTGGA ::: AACTCTTAGA 770  580 AGAAAAAGAC ::::: ATTAAATGTC 830	TGGAGTGGAT :::: AAGTGCCA 780 690 AAGGATAG ::::: AACTGCCACG 840 750 AGGACGAGCT	GAAGTGGCGAA : :::::: : GGAGTGGCAAT 790 700 TAAGCTTGAAA ::: ::: CAAGTGA 760 AAAGAAAGTGT	:::::: GAAGAAAAAATO 800 710 AAGCCCTAAAGO :::::: -TGGCAGAAAG- 850 770 GTTCAACT	GCTCAGAACGAC  :::::  FATGGCTCTACT  810  720  GCTCAGAACGAC  ::::::::: TCAACTCCAT
 649550  7	AAGGCGA ::: :: AAGATGA 760  6 AAA : : CACACCA 820  30 CTGATCT ::::	ATGAGGTGGA  ::: AACTCTTAGA 770  580 AGAAAAAGAC ::::: ATTAAATGTC 830  740 CGGAACATCA	TGGAGTGGAT :::: AAGTGCCA 780 690 AAGGATAG :::: AACTGCCACG 840 750 AGGACGAGCT ::::	GAAGTGGCGAA : ::::::: GGAGTGGCAAT 790  700 TAAGCTTGAAA ::: ::: CAAGTGA 760 AAAGAAAGTGT : :::::	:::::::  GAAGAAAAAATO  800  710  AAGCCCTAAAGO ::::::  TGGCAGAAAG- 850  770  GTTCAACT	GATGGCTCTAAA  ::::  SATGGCTCTACT  810  720  GCTCAGAACGAC  ::::::  -TCAACTCCAT  860  780  AATGACCTGA
649550 7649550	AAGGCGA ::: :: AAGATGA 760  6 AAA : : CACACCA 820  30 CTGATCT ::: TACATTT 870  790 AGGAGCT	ATGAGGTGGA  1::: AACTCTTAGA 770  580 AGAAAAAGAC 1::::: ATTAAATGTC 830  740 CGGAACATCA 1:::::: CGGCAGCA 880  AGCTCATCTT	TGGAGTGGAT  :::: AAGTGCCA 780  690 CAAGGATAG :::: CAACTGCCACG 840  750 AGGACGAGCT :::: CGGATATAACA 890  CCAACAAGCAG	GAAGTGGCGAA : :::::: GGAGTGGCAAT 790  700 TAAGCTTGAAA ::: ::: CAAGTGA 760 AAAGAAAGTGT : ::: :: GAGTAAAGATT 900 CAAGTG	::::::  GAAGAAAAAAT  800  710  AAGCCCTAAAG  ::::::  -TGGCAGAAAG- 850  770  GTTCAACTA ::::::  GTACAGCTGTTA  910  820  CCTTCTGGGGAA	GATGGCTCTAAA  ::::  GATGGCTCTACT  810  720  GCTCAGAACGAC  :::::: TCAACTCCAT  860  780  AATGACCTGA  ::::::  ACTGCAACATGG
649550 7649550	AAGGCGA ::: :: AAGATGA 760  6 AAA : :: CACACCA 820  30 CTGATCT ::: TACATTT 870  790 AGGAGCT :: ::	ATGAGGTGGA  : :: AACTCTTAGA  770  580 AGAAAAAGAC  ::: :: ATTAAATGTC  830  740 PGGAACATCA  :: :: :: PGGCAGCA  880  800  CACTCATCTT	TGGAGTGGAT  :::: AAGTGCCA 780  690 CAAGGATAG ::::: CAACTGCCACG 840  750 AGGACGAGCT :::: AGGATATAACA 890  CCAACAAGCAG ::::::	GAAGTGGCGAA  : :::::: GGAGTGGCAAT  790  700  TAAGCTTGAAA  ::: ::: CAAGTGA  760  AAAGAAAGTGT  : :::: GAGTAAAGATT  900 CAAGTG  : :::	:::::::  GAAGAAAAAAT( 800  710  AAGCCCTAAAG( ::::::  -TGGCAGAAAG- 850  770  GTTCAACT :::::::  GTACAGCTGTTA 910  820  CCTTCTGGGGAA ::::::::	GATGGCTCTAAA  ::::  GATGGCTCTACT  810  720  GCTCAGAACGAC  :::::: TCAACTCCAT  860  780  AATGACCTGA  :::::::  ACTGCAACATGG  920  830  GTCGGCGATCTT
- 7 649550 - 649550 -	AAGGCGA ::: :: AAGATGA 760  6 AAA : :: CACACCA 820  30 CTGATCT ::: TACATTT 870  790 AGGAGCT :: :: AGCTGAT 930  840	ATGAGGTGGA  1::: AACTCTTAGA  770  580 AGAAAAAGAC  1::::: ATTAAATGTC  830  740 PGGAACATCA  1:::::: PGGC-CAGCA  880  PACTCATCTT  1::::: PGTCCATGCT  940  860  860  860  860  860  860  860  8	TGGAGTGGAT  :::: AAGTGCCA 780  690 AAGGATAG :::: AACTGCCACG 840  750 AGGACGAGCT :::: AGGATATAACA 890  CCAACAAGCAG ::::: AAAGATAAAG 950  810 810 810 810 810 810 810 810 810 8	GAAGTGGCGAA  : :::::: GGAGTGGCAAT  790  700  TAAGCTTGAAA  ::: ::: CAAGTGA  760  AAAGAAAGTGT: ::::: GAGTAAAGATT  900 CAAGTG : ::: GTGATCTGGTA  960	::::::  GAAGAAAAAAT  800  710  AAGCCCTAAAG  ::::::  -TGGCAGAAAG- 850  770  GTTCAACT ::::::  GTACAGCTGTTA  910  820  CCTTCTGGGGAG  ::::::  CCAT-TACACAA  970  870  CGGTGCCCTCC	GATGGCTGTTCTAAA  ::::  GATGGCTCTACT  810  720  GCTCAGAACGAC  :::::: TCAACTCCAT  860  780  AATGACCTGA  ::::::  ACTGCAACATGG  920  830  GTCGGCGATCTT  ::::::  ATGCCTGTTCTT
- 7 649550 - 649550 - 649550	AAGGCGA ::: :: AAGATGA 760  6 AAA : :: CACACCA 820  30 CTGATCT ::: TACATTT 870  790 AGGAGCT :: :: AGCTGAT 930  840GGACC :: ::	ATGAGGTGGA  1::: AACTCTTAGA  770  S80 AGAAAAAGAC  1::::: ATTAAATGTC  830  740 PGGAACATCA  880  PACTCATCTT  1:::: PGTCCATGCT  940  800  800  800  800  800  800  800	TGGAGTGGAT  :::: AAGTGCCA 780  690 AAGGATAG :::: AACTGCCACG 840  750 AGGACGAGCT :::: AGGATATAACA 890  CCAACAAGCAG ::::: AAAGATAAAG 950  AGGCCGATGC :::: AACTGCACTT	GAAGTGGCGAA  : :::::: GGAGTGGCAAT  790  700  TAAGCTTGAAA  ::: ::: CAAGTGA  760  AAAGAAAGTGT : :::: GAGTAAAGTGT : :::: GAGTAAAGATT 900 CAAGTG : ::: GTGATCTGGTA 960  60 ATGGTGTT :::: TTGGTCAAGCA	::::::  GAAGAAAAAAT  800  710  AAGCCCTAAAG  ::::::  -TGGCAGAAAG- 850  770  GTTCAACT ::::::  GTACAGCTGTTA  910  820  6CCTTCTGGGGAG  :::::::  CCAT-TACACAA  970  870  670  670  670  670  670  670  6	TCTAAA  ::::  GATGGCTCTACT  810  720  GCTCAGAACGAC  ::::::  -TCAACTCCAT  860  780  AATG-ACCTGA  ::::::  ACTGCAACATGG  920  830  GTCGGCGATCTT  ::::::  ATGCCTGTTCTT  980  880  GTCCCTGCGAGG

_		GTGGCAATT	CACTCCTCTTC	: ::: : :: ATGAG-GCAGCT 70 108	TTCTAAGAACA	AGGGTTGAAGTA
649550	ACTGC-C	TGGACCAAGT	rgtatggtcaa	980 GACACAGACACO	CCAACCG	GAAG
-	TGTTCTC	TTCTCTTAAC	GTTATGGTGCA		rgctcaattg1	rcacaataaaag
649550		GAGTGGGTA	ACCCCAAAGGA		rctcttacct(	1040 CAAGAAATTGAA
- 11	TGCTATA	GACTTGGCT	CCACACCACA		GATTAGCAT	TATGAATTTAAA
649550	1050 GGTTAAA		AAACAGGAC		rcccccca	1080 AGAAACCAGCGC : ::: :: :
-	GGCCACT	CGTTGCTGC	AAGCTGCACGA		TACTCGAATC <i>I</i>	AAAAAACATCTC
	-CTCCG-	TGGCGG	CCACGCCT		ACAGCCI	1130 FCGGCTCCTGCT
_	TCTCTGG	AAATGGTGAA	ATTTCAAGCAT		TGAAACAGCAT	TTGCATTGTGCT
649550	GCTGTGA	ACTCC-TCT	GCTTCAGCAGA	1170 TAAGCCATTATO	CCAACATGAAG	GATCCTGACTCT
	GCTGC-A	TCTCCATAT		-AAGCAAATAT-	GTGAA-	::: :: CTGTTGCT 1380
649550		CTGTCCCGG	AACAAGGATGA	AGTGAAGGCC	-ATGATTGAGA	0 1250 AAACTCGGGGGG
649550 -	CGGGAAG	CTGTCCCGG! ::: GDGG!	AACAAGGATGA : ::: :: : AGCAAACATCA	AGTGAAGGCC	-ATGATTGAGA : :: : AAAGAATTCTT	AAACTCGGGGGG ::::::::::::::::::::::::::::::
_	CGGGAAG : :: AAGAAAA 1390	CTGTCCCGGA :::GGA  1260CGGGGACG	AACAAGGATGA : ::: :: : AGCAAACATCA 1400  1270 GGCCAACAAGG	AGTGAAGGCC: ::::::: ATGAAAAGACTA 1410  1280 CCTTCCCT	-ATGATTGAGA : :: : AAAGAATTCTT 1420  12GTGCA	AAACTCGGGGGG ::::::::::::::::::::::::::::::
- 649550 -	CGGGAAG : :: AAGAAAA 1390  AAGTTGA : ::	CTGTCCCGGA	AACAAGGATGA : ::: :: : AGCAAACATCA 1400  1270  GGCCAACAAGG :: ::: : AGCTCATAATG	AGTGAAGGCC : :: : : ATGAAAAGACTA 1410  1280 CCTTCCCT : :	-ATGATTGAGA : :: : AAAGAATTCTT 1420  12GTGCA ::: : GTAGTGGTGAA	AAACTCGGGGGG :::: : FGACTCCTCTGC 1430
- 649550 -	CGGGAAG : ::  AAGAAAA 1390  AAGTTGA : :: :  ACGTGGC: 1440  1300 AAA	CTGTCCCGGA  :::GGA  1260CGGGGACC :::: ATCTGAGAAA  1450  1310 GGAGGTGGA	AACAAGGATGA : ::: :: : AGCAAACATCA 1400  1270 GGCCAACAAGG :: :::: AGCTCATAATG 1460  1320 AAAGATGAATA	AGTGAAGGCC : :: : : ATGAAAAGACTA 1410  1280 CCTTCCCT : : ATGTTGTTGAAG 1470  AGA	-ATGATTGAGA : :: : AAAGAATTCTT 1420  12GTGCA ::: : GTAGTGGTGAA	AAACTCGGGGGG :::: : FGACTCCTCTGC 1430  290 ATCA-GCACCAA ::: : ::: AACATGAAGCAA 1490  1330 -AGATGGAGGAA
- 649550 - 649550	CGGGAAG : ::  AAGAAAA 1390  AAGTTGA : :: :  ACGTGGC: 1440  1300  AAA : ::  AGGTTAA	CTGTCCCGGA  :::GGA  1260CGGGGACC :::: ATCTGAGAAA 1450  1310 GGAGGTGGAC ::::: TGCTCTGGA	AACAAGGATGA : ::: :: : AGCAAACATCA 1400  1270 GGCCAACAAGG :: : :: : AGCTCATAATG 1460  1320 AAAGATGAATA :: : :	AGTGAAGGCC : :: : : ATGAAAAGACTA 1410  1280 CCTTCCCT : : ATGTTGTTGAAC 1470  AGA	-ATGATTGAGA : :: : AAAGAATTCTT 1420  12GTGCA ::: : GTAGTGGTGAA 1480 CACAGAGCTGCA	AAACTCGGGGGG :::: : FGACTCCTCTGC 1430  290 ATCA-GCACCAA ::: : ::: AACATGAAGCAA 1490  1330 -AGATGGAGGAA ::: : ::: CATATTGTGGTC
- 649550 - 649550	CGGGAAG : ::  AAGAAAA 1390  AAGTTGA : :: :  ACGTGGC 1440  1300 AAA : ::  AGGTTAA 1500  1340 GTAAAGG	CTGTCCCGGA  :::GGA  1260CGGGGACC :::: ATCTGAGAAA  1450  1310 GGAGGTGGAA  ::::: TGCTCTGGA	AACAAGGATGA : :: : :: : AGCAAACATCA 1400  1270 GGCCAACAAGG :: : :: : AGCTCATAATG 1460  1320 AAAGATGAATA :: : : FAATCTTGGTC 1520  1350 CCAACATCCGA	AGTGAAGGCC : :: : : ATGAAAAGACTA 1410  1280 CCTTCCCT : : ATGTTGTTGAAC 1470  AGA AGACTTCTCTAC 1530  1360 1360 1360 1360 1360 1360 1360	-ATGATTGAGA : :: : AAAGAATTCTT 1420 GTGCA ::: : GTAGTGGTGAA 1480 CACAGAGCTGC 1540  370 GGACTT	AAACTCGGGGGG :::: : FGACTCCTCTCC 1430  290 ATCA-GCACCAA ::: : ::: AACATGAAGCAA 1490  1330 -AGATGGAGGAA ::: ::: CATATTGTGGTC 1550
- 649550 - 649550 -	CGGGAAG : ::  AAGAAAA 1390  AAGTTGA : :: :  ACGTGGC 1440  1300 AAA : ::  AGGTTAA 1500  1340 GTAAAGG : :  ATCTACA	CTGTCCCGGA  :::GGA  1260CGGGGACC :::: ATCTGAGAAA  1450  1310 GGAGGTGGAA  ::::: TGCTCTGGAA  1510  AAGC ::: AACCTGCCGG	AACAAGGATGA : :: : :: :: AGCAAACATCA 1400  1270 GGCCAACAAGG :: : :: :: AGCTCATAATG 1460  1320 AAAGATGAATA :: : :: FAATCTTGGTC 1520  1350 CCAACATCCGA :: : : :: CCTACTCCTGA	AGTGAAGGCC : :: : : ATGAAAAGACTA 1410  1280 CCTTCCCT : : ATGTTGTTGAAC 1470  AGA ::: AGACTTCTCTAC 1530  1360 1360 1361 : : : : : :	-ATGATTGAGA : :: : AAAGAATTCTT 1420 GTGCA ::: : GTAGTGGTGAA 1480  CACAGAGCTGC 1540  370 GGACTT : : : GATCCTAACAS	AAACTCGGGGGG :::: : FGACTCCTCTGC 1430  290 ATCA-GCACCAA ::: : :::: AACATGAAGCAA 1490  1330 -AGATGGAGGAA ::: : ::: CATATTGTGGTC 1550
- 649550 - 649550 - 1	CGGGAAG : ::  AAGAAAA 1390  AAGTTGA : :: :  ACGTGGC 1440  1300 AAA : ::  AGGTTAA 1500  1340 GTAAAGG : :  ATCTACA 1560  380 AGGACGT	CTGTCCCGGA  :::GGA  1260CGGGGACC ::::: ATCTGAGAAA 1450  1310 GGAGGTGGAA ::::: TGCTCTGGAA 1510  AAGC :: AACCTGCCGC 1370  1390 CTCCGCCTCC	AACAAGATGA : :: : :: : AGCAAACATCA 1400  1270 GGCCAACAAGG :: : :: : AGCTCATAATG 1460  1320 AAAGATGAATA :: : : FAATCTTGGTC 1520  1350 CCAACATCCGA :: : : :: CCTACTCCTGA 1580  1400 CACCAAGAGCC	AGTGAAGGCC	-ATGATTGAGA : :: : AAAGAATTCTT 1420 GTGCA :: :: : GTAGTGGTGAA 1480	AAACTCGGGGGG ::::::::::::::::::::::::::::::
- 649550 - 649550 - 1649550	CGGGAAG : ::  AAGAAAA 1390  AAGTTGA : :: :  ACGTGGC 1440  1300 AAA : ::  AGGTTAA 1500  1340 GTAAAGG : :  ATCTACA 1560  380 AGGACGT ::: ::	CTGTCCCGGA  :::GGA  1260CGGGGACC :::: ATCTGAGAAA  1450  1310 GGAGGTGGAA  ::::: TGCTCTGGAA  1510  AAGC :: AACCTGCCGC  1390 CTCCGCCTCC	AACAAGGATGA : :: : :: : AGCAAACATCA 1400  1270 GGCCAACAAGG :: : :: : AGCTCATAATG 1460  1320 AAAGATGAATA :: : : FAATCTTGGTC 1520  1350 CCAACATCCGA :: : : :: CCTACTCCTGA 1580  1400 CACCAAGAGCC : : : :	AGTGAAGGCC : :: : : : ATGAAAAGACTA 1410  1280 CCTTCCCT : : ATGTTGTTGAAC 1470  AGA ::: AGACTTCTCTAC 1530  1360 1360 1360 1360 1376TGTGTCTGAC : : : : : GCTATGGGTGTC 1590  1470  1470  1470  1570  1470  1470	-ATGATTGAGA : :: : AAAGAATTCTT 1420 GTGCA :: :: GTAGTGGTGAA 1480  CACAGAGCTGC 1540  370 GGACTT : : : GATCCTAACAT 1600  410 14 CAGGAGTTGTT : : : : CAGCAACTCCT	AAACTCGGGGGG ::::::::::::::::::::::::::::::

649550	O TCTTGT	CCCCTTO	GGGGGCAGA	G	GTG-AAG(	SCAGAGCCTGTT	GAAG
						SCAGAGCCTGTT ::::::: SCAAAGGCTGGA	
_	1680		1700				
					1510		
64955						CCAAAAAAAAGC- ::::::::	
_	TCGAAA	CTGTAAAAA	ACTGTGTAC	TGTTCAGAG-	-TGTCAACT(	CAGAGACATTG	
	1740	1750	1760	1770	1780	1790	
61955	0 · GC					1560 CTGAAAAGAGA	
04933	::	:	:::	: :: :::	:::::::	:: :	::
_			ACTTCATTTT 1820			G-TGTCCGTGG- 340 1	-TGG 850
					1610		-
64955						rggactgga :::: :::	
_		CTGCTACAGO 1860			TAAAGATAA 1890	AGGAGGCCTTGT 1900	AC-C
		1630	1640		1650		•
64955			CCTGGA	GAAAG		GTCTT	
_	TTTGCA	CAATGCATG'	TTTTATGGA	CATTATGAAG	TTGCAGAACT	TTCTTGTTAAAC	ATGG
1:	910	1920	1930	1940	1950	1960	
C4055					1690		
64933						AGGAACCAACTC	
- 1			AGCTGATTTA 1990			ATGAAGCAGCAG 2020	CAAA
				-	1730	17	40
64955	0		-TACAAGCTG	CAGCTTC	-TGGAGGA-	CGAC-AAGG	AAAA
	AGGAAA	ATATGAAAT'				: :: :: ACCCTACCAAAA	•
_ 2	030	2040	2050	2060	2070	2080	
			1760				
64955						CGGTG : : :	
- 2		TGGAAATAC'		CTTGTTAAAG		CAGATATTCAAC	
						2140	•
	790	180	00 18	10 10		1830	
			AACTGGAACA			GCCATI	GAGC
	0 GTAG : :::	CAACA	: :: :	GATGCCGTCC	CAAGGAGGAT	GCCATT	: :
- 2	0 GTAG : :::	CAACA : : :GGGAGATGC	: :: : AGCTTTGCTA	GATGCCGTCC	CAAGGAGGAT	GCCATI	: :
_	0 GTAG : ::: GCTTAG 150	CAACA : :GGGAGATGC 2160 1840	: :: : AGCTTTGCTA 2170	GATGCCGTCC ::::: ::: GATGCTG-CC 2180  1850	CAAGGAGGAT ::: ::: : CAAGAAGGGT 2190	GCCATT :::: FGTTTAGCCAGA 2200 1860	: : GTGA
_	0 GTAG : ::: GCTTAG 150	CAACA : :GGGGAGATGC 2160 1840 CTTC	: :: : AGCTTTGCTA 2170	GATGCCGTCC :::::::::::::::::::::::::::::::	AAGGAGGAT :::::::: CAAGAAGGGT 2190 -ATAT	GCCATT :::: FGTTTAGCCAGA 2200 1860 -GAAGAAAA	: : GTGA
64955	0 GTAG : ::: GCTTAG 150  0 A : AGAAGT	CAACA : :GGGGAGATGC: 2160 1840 CTTC ::::	: :: : AGCTTTGCTA 2170ATG- ::: CTGATAATGT	GATGCCGTCC :::::::::::::::::::::::::::::::	CAAGGAGGAT  CAAGAAGGGT  2190  ATAT  CGATACCCAA	GCCATT :::: FGTTTAGCCAGA 2200  1860 -GAAGAAAA :::::::::	: : GTGA AACC : :
64955	0 GTAG : ::: GCTTAG 150 0 A	CAACA : :GGGGAGATGC: 2160 1840 CTTC	: :: : AGCTTTGCTA 2170ATG- ::: CTGATAATGT	GATGCCGTCC :::::::::::::::::::::::::::::::	CAAGGAGGAT  CAAGAAGGGT  2190  ATAT  CGATACCCAA	GCCATT :::: FGTTTAGCCAGA 2200  1860 -GAAGAAAA :::::::::	: : GTGA AACC : :
64955 	0 GTAG : ::: GCTTAG 150  0 A : AGAAGT 2210 1870	CAACA : :GGGAGATGC 2160 1840 CTTC :::: TGTCTTCTC 2220	E:::::AGCTTTGCTA 2170 ATG- ::: CTGATAATGT 2230	GATGCCGTCC :::::::::::::::::::::::::::::::	AAGGAGGAT  ::::::: CAAGAAGGGT  2190  -ATAT  ::: CGATACCCAAC  2250	GCCATT :::: FGTTTAGCCAGA 2200  1860 -GAAGAAAA ::::::::::::::::::::::::::	: : : .GTGA .AACC : : : .ACAC
64955 	0 GTAG : ::: GCTTAG 150  0 A : AGAAGT 2210  1870 0 GGGAAC ::	CAACA : GGGAGATGC 2160  1840CTTC :::: TGTCTTCTCC 2220  1880 GCTTGGCAC :::::	: :: : : AGCTTTGCTA 2170 ATG- ::: CTGATAATGT 2230 TCCAA : ::	GATGCCGTCC :::::::::::::::::::::::::::::::	CAAGGAGGAT  CAAGAAGGGT  2190  ATAT  CATACCCAAC  2250  1900  CAAGTATCCCACC  CAAGTATCCCCCCCCCCCCCCCC	GCCATT ::::  FGTTTAGCCAGA 2200  1860 -GAAGAAAA ::::::::  FGCAGACATTCA 2260  1910  AAAAAAGTTCAA	: : : GTGA  AACC : : : ACAC  920 CCCC :
64955	0 GTAG : ::: GCTTAG 150  0 A : AGAAGT 2210  1870 0 GGGAAC ::	CAACA : GGGAGATGC 2160  1840CTTC :::: TGTCTTCTC 2220  1880 GCTTGGCAC ::::: CATTTAGCAG	: :: : : AGCTTTGCTA 2170 ATG- ::: CTGATAATGT 2230 TCCAA : :: CTGGTTATAA	GATGCCGTCC :::::::::::::::::::::::::::::::	CAAGGAGGAT  CAAGAAGGGT  2190  ATAT  CATACCCAAC  2250  1900  CAAGTATCCCACC  CAAGTATCCCCCCCCCCCCCCCC	GCCATT ::::  FGTTTAGCCAGA 2200  1860 -GAAGAAAA ::::::::  FGCAGACATTCA 2260  1910 AAAAAGTTCTAC AGTATTTGTTAC	: : : GTGA  AACC : : : ACAC  920 CCCC :

649550	1930 TGGAGATTGACTA			1950 AGGCAG
_			AGGACTTATTCCTT	: :::: TTACATAATGCAGCATC 2380
649550		TGAAGAAGCTG		CCTGGCACCAA
_		TGTAGCAGCTCTACT	AATAAAGTATAATO	: :: :: ::: CCATGTGTCAATGCCAC ) 2440
649550	GTCCAAGCTCC		AC-CTCATCAAGAT	GATCTTT
-	GGACAAATGGGCTTTC	C-ACACCTTTGCACG	AAGCAGCCCAAAA	GGACGAACACAGCTTT
649550	: ::::::::	::: ::	:::	CCATGGTGGAGTA
_		2530	2540 255 2090 210	
649550	TGAGATCGACCTT	CAGAAGATG	CCCTTGGGGAA	AGCTGAGCAAAAGGCAG
-	2570 2580	2590	2600 263	
649550			TCCTCAGTGAG	STCCAGCAGGCGGTGTC
_				GTG-AGAAGCCCAGGAG 2670 2680
649550	TCAGGGCAGCAGCGA		GGATCTCTCAAAT	2210 CGCTTTTACACCCTG-A
_	CCACTGCAGATGCTC 2690 2	TCTCTTCAGGTCCAT	CTAGCCCATCAAGG 2720	CCTTTCTGCAGCCAGCA 2730 2740
		-TGGGATGAAG	AAGCCTCCGCT	CCTGAA
_	GTCTTGACAACTTAT	CTGGGAGTTTTCAG		: ::: AGTTAGTTCAAGTGGAA 2790 2800
2 649550	CAATGCAGACA	0 2280 GTGTGCAGGCCAAGG :: :: :: :::		·
_		GTTTGGAGAAAAAGG 820 2830	AGGTTCCAGGAGT 2840	AGATTTTAGCATAACTC 2850 2860
			TGCTGGACATCGA	2320 2330 GGTG-GCCTACAGTCTG
-			: :::: :: TAATGGATATATT 2900	: : : :::: IGAGAGAGAACAGATCA 2910 2920
649550		GATGATAGCAG		GATG <b>-</b> TCAAC
-	CTTTGGAT-GTATTA			GAGATTGGAATCAATGC 2970 2980

238 649550 -	TATGAGA	AGCTCAAAAC	TGACATTAAG	GTGGTTGACA	2420 GAGAT-TCTGA	AAGAAGCCG
T	TATGGACATAC	GCACAAA-C		GGAGTCGAGA	GACTTATCTC	CGGACAACA
	2440 AGATCATCAGGA	AGTATGTTA	AGAACA		TGCAACCACA	:
·P	AGGTCTTAACCO	CA-TAT-TTA	ACTTTGAACA	CCTCTGGTAG	TGGAACAATT	CTTATAGAT 3090
649550 -					AGT	500 -CATCGA :: ::::
_	CTGTCTCCTGAT	rgataaagag	TTTCAGTCTG	TGGAGGAAGA	GATGCAAAGT	ACAGTTCGA
649550 T	TATCTTTAAGAT	TAGAGCGT	GAAGGCGAA-	TGCCAGCG	2550 TTACAAGCC-0	CTTT
_	SAGCACAGAGAT 3160	TGGAGGTCAT	GCAGGTGGAA	TCTTCAACAG	ATACAATATT	CTCAAGATT
	2560 AAGCAGCTTCAT	TAACCGAAGA		ACGGGTCCA-		
	CAGAAGGTTTGT		AA-CTATGGG	AAAGATACAC		
649550 -		CCACCAACTT	TGCTG	-GGATCCTGT	263	TTCG
	rctgaagaaaa	CCAC-AACCA	TGCCAATGAA .3300	CGAATGCTAT 3310		rccttttgt
	26 GATAC :: ::			GCGCCCGTG-		CATGTTTGG
	SAATGCAATTAT	rccacaaagg	CTTTGATGAA	AGGCATGCGT		TATGTTTGG
649550 T	2680 2 TAAAGGGATCTA	ATTTCGCTGA	CATGGTCTCC		ACTACTGCCA	
_ F	AGCTGGCATTTA 3400	ATTTTGCTGA	AAACTCTTCC	AAAAGCAA	TCAATATGTA'	
649550	2740 2 GGGAGACCCAAT	PAGGCTTAAT	CCTGTT	GGGAGAAG		GGAAACATG
_ (	GGAGGAGGTACT 3460	rgggtgt		AAGACAGATO	TTGTTACATT	
	2790 2 FATGAACTGA	AAGCACGCTT	CACATATCAG	CAAGTTAC	CCCAA	GGGCAAGCA
(	CAGCTGCTCTT	rtgc-cgggt	AACCT-TGGG		CTGCAGTTCA	
	340 285 CAGTGTCAAAG		2860 GGCAAAACTA		CCTTCAG	
	: :: :: : AAATGGCACAT	: :	: :: :::	: ::: :	:: :::	

	3570	3580	3590	3600	3610	3620
	2880 -CTAACAT'	2890 TAGTCTGGAT	2900 CGTGTAGAC	2910 STTCCTCTT(	2920 GGACCGGGATT	2930 TCATCTGGTGTG
013000	::: :::	::: ::: ::	::	:: :	: :: : :: ::	::: :::
-	CCTAGCAT 3630	TAG-CTGAAT 364		-TTACAGAG0 3650	SAGAACAGGCTT 3660	ATCCTGAGTA 3670
	2940	2950	2960	2	2970	2980
649550	AATGACAC	CTCTCTACTA	ATATAACGAG'	rac	-ATTGTCTATG-	ATATTGCTCA
	: :	:: :::::	::::::	:	:: ::: :::	: :: : :
-	TTTAATTA 3680	CTTACC <i>I</i> 3690	AGATTATGAGO 3700	GCCTGAAGG1 371(		ATAAATAGTTAT 3730
	2990	3000	3010	3020	)	
649550	GGTAAATC	TGAAGTAI	CTGCTGAAA	CTGAAAT1	ГСАА	т
	:::	:: :: :	: :::::	:: ;:::: :	::::	:
_						TGGCCTCTACGT
	3740	37	750 3	760	3770 37	80 3790
	3030	3040		•		
649550		CTCCCTGTGG	STAA			
	:::: :	: :::	::			
-	TTTACTCC 38	TTTGCTGAAA 00 38	AAAAAAAAA 810		,	